



SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: DeBonte, Lorin R. Fan, Zhegong Loh, Willie H-T. Shorrosh, Basil S.
- (ii) TITLE OF THE INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/874,109
 - (B) FILING DATE: 12-JUN-1997 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US96/20090
 - (B) FILING DATE: 13-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ronald C. Lundquist
 - (B) REGISTRATION NUMBER: 37,875
 - (C) REFERENCE/DOCKET NUMBER: 07148/063001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

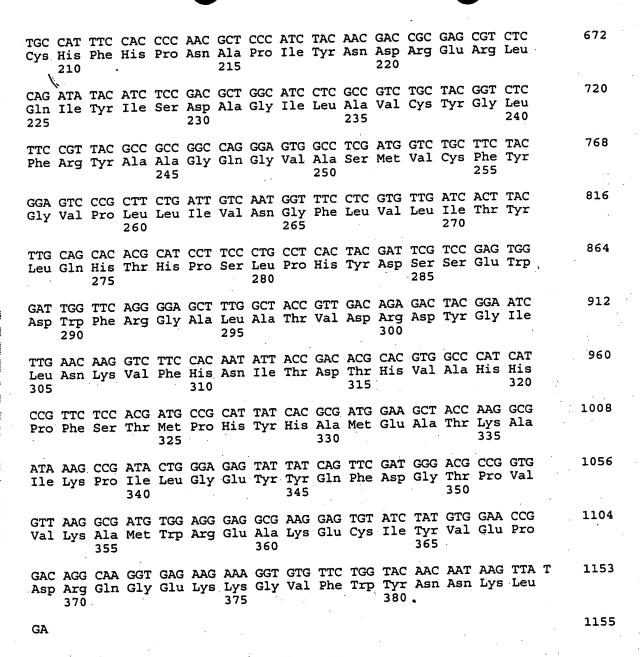


(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Brassica napus

(ix) FEATURE:
(D) OTHER INFORMATION: Wild type Fad2.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

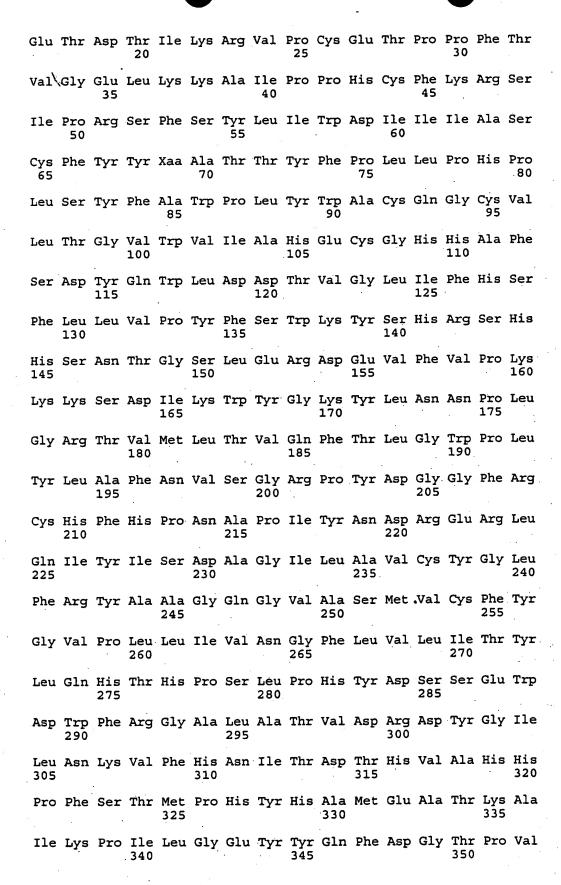
| | (XI) | SE | SOFIAC | | | | | | | | | | | | | | |
|----------------|-----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|-----|
| ATO Met | GGT Gly | GCA Ala | GGT Gly | GGA Gly 5 | AGA Arg | ATG Met | CAA Gln | GTG Val | TCT Ser 10 | CCT Pro | CCC Pro | TCC Ser | AAG Lys | AAG Lys 15 | TCT Ser | | 48 |
| GAZ Glu | A ACC | GAC Asp | ACC Thr 20 | ATC Ile | AAG Lys | CGC Arg | GTA Val | CCC Pro 25 | Cys | GAG Glu | ACA Thr | CCG Pro | CCC Pro 30 | TTC Phe | ACT Thr | | 96 |
| GT(Va | GGA Gly | GAA Glu 35 | CTC Leu | AAG Lys | AAA Lys | GCA Ala | ATC Ile 40 | CCA Pro | CCG Pro | CAC His | TGT Cys | TTC Phe 45 | AAA Lys | CGC Arg | TCG Ser | | 144 |
| ATC Ile | C CCT Pro 50 | CGC Arg | TCT Ser | TTC. Phe | TCC Ser | TAC Tyr 55 | CTC Leu | ATC Ile | TGG Trp | GAC Asp | ATC Ile 60 | ATC Ile | ATA Ile | GCC Ala | TCC Ser | | 192 |
| TG(Cy: | TTC Phe | TAC Tyr | TAC Tyr | NTC Xaa | GCC Ala 70 | ACC Thr | ACT Thr | TAC Tyr | TTC Phe | CCT Pro 75 | CTC Leu | CTC Leu | CCT Pro | CAC His | CCT Pro 80 | • ', | 240 |
| CT Le | TCC Ser | TAC Tyr | TTC Phe | GCC Ala 85 | TGG Trp | CCT Pro | CTC Leu | TAC Tyr | TGG Trp 90 | GCC Ala | TGC Cys | CAA Gln | GGG Gly | TGC Cys 95 | GTC Val | | 288 |
| CT. Le | A ACC 1 Thr | GGC Gly | GTC Val 100 | TGG Trp | GTC Val | ATA Ile | GCC Ala | CAC His 105 | GAA Glu | TGC Cys | GGC Gly | CAC | CAC His 110 | GCC Ala | TTC Phe | | 336 |
| AG Se | C GAC r Asp | TAC Tyr 115 | Gln | TGG Trp | CTT Leu | GAC Asp | GAC Asp 120 | ACC Thr | GTC Val | GGT Gly | CTC Leu | ATC Ile 125 | Phe | CAC His | TCC Ser | | 384 |
| TT Ph | C CTC e Leu 130 | Leu | GTC Val | CCT Pro | TAC Tyr | TTC Phe 135 | Ser | TGG Trp | AAG Lys | TAC Tyr | AGT Ser 140 | His | CGC Arg | AGC Ser | CAC | | 432 |
| CA Hi 14 | | AAC Asn | ACT Thr | GGC Gly | TCC Ser 150 | CTC Leu | GAG Glu | AGA Arg | GAC Asp | GAA Glu 155 | Val | TTT Phe | GTC Val | CCC | AAG Lys 160 | a. | 480 |
| AA Ly | G AAG s Lys | TCA Ser | GAC Asp | ATC Ile 165 | Lys | TGG Trp | TAC Tyr | GGC Gly | AAG Lys 170 | Tyr | CTC Leu | AAC Asn | AAC Asn | CCT Pro 175 | Leu | | 528 |
| GC G1 | A CGC y Arg | ACC | GTG Val | Met | TTA Leu | ACG Thr | GTT Val | CAG Gln 185 | Phe | ACT Thr | CTC Leu | GGC Gly | TGG Trp 190 | Pro | TTG Leu | | 576 |
| TA Ty | C TTA | GCC Ala | Phe | Asn | .Val | TCG Ser | Gly | Arg | CCT | TAC | GAC Asp | GGC Gly 205 | Gly | TTC Phe | CGT Arg | | 624 |



(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser





Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Brassica napus
- (ix) FEATURE:
- (D) OTHER INFORMATION: G to A transversion mutation at nucleotide 316.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | (141) | 024 | (| | | | | | | | | | | | | • . | |
|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|-----|
| ATG Met 1 | GGT Gly | GCA Ala | GGT Gly | GGA Gly 5 | AGA Arg | ATG Met | CAA Gln | GTG Val | TCT Ser 10 | CCT Pro | CCC Pro | TCC Ser | AAG Lys | AAG Lys 15 | TCT Ser | | 48 |
| GAA Glu | ACC Thr | GAC Asp | ACC Thr 20 | ATC Ile | AAG Lys | CGC Arg | GTA Val | CCC Pro 25 | TGC Cys | GAG Glu | ACA Thr | CCG Pro | CCC Pro 30 | TTC Phe | ACT Thr | | 96 |
| GTC Val | GGA Gly | GAA Glu 35 | CTC Leu | AAG Lys | AAA Lys | GCA Ala | ATC Ile 40 | CCA Pro | CCG Pro | CAC His | TGT Cys | TTC Phe 45 | AAA Lys | CGC Arg | TCG Ser | | 144 |
| ATC Ile | CCT Pro 50 | CGC Arg | TCT Ser | TTC Phe | TCC Ser | TAC Tyr 55 | CTC Leu | ATC Ile | TGG Trp | GAC Asp | ATC Ile 60 | ATC Ile | ATA Ile | GCC Ala | TCC | | 192 |
| TGC Cys 65 | TTC Phe | TAC Tyr | TAC Tyr | NTC Xaa | GCC Ala 70 | ACC Thr | ACT Thr | TAC Tyr | TTC Phe | CCT Pro 75 | Leu | CTC Leu | CCT | CAC His | CCT Pro 80 | | 240 |
| CTC Leu | TCC Ser | TAC Tyr | TTC Phe | GCC Ala 85 | TGG Trp | CCT Pro | CTC Leu | TAC Tyr | TGG Trp 90 | GCC Ala | TGC Cys | CAA Gln | GGG Gly | TGC Cys 95 | GTC Val | | 288 |
| CTA Leu | ACC Thr | GGC Gly | GTC Val 100 | TGG Trp | GTC Val | ATA Ile | GCC Ala | CAC His 105 | AAG Lys | TGC Cys | GGC Gly | CAC His | CAC His 110 | GCC Ala | TTC Phe | | 336 |
| AGC Ser | GAC Asp | TAC Tyr 115 | CAG Gln | TGG Trp | CTT Leu | GAC Asp | GAC Asp 120 | Thr | GTC Val | GGT | CTC Leu | ATC Ile 125 | TTC Phe | CAC His | TCC Ser | | 384 |

| TTC Phe | CTC Leu 130 | CTC Leu | GTC Val | CCT Pro | TAC Tyr | TTC Phe 135 | TCC Ser | TGG Trp | AAG Lys | TAC Tyr | AGT Ser 140 | CAT His | CGC Arg | AGC Ser | CAC His | | 432 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----|------|
| CAT | TCC Ser | AAC Asn | ACT Thr | GGC Gly | TCC Ser 150 | CTC Leu | GAG Glu | AGA Arg | GAC Asp | GAA Glu 155 | GTG Val | TTT Phe | GTC Val | CCC Pro | AAG Lys 160 | | 480 |
| AAG Lys | AAG Lys | TCA Ser | GAC Asp | ATC Ile 165 | AAG Lys | TGG Trp | TAC Tyr | GGC Gly | AAG Lys 170 | TAC Tyr | CTC Leu | AAC Asn | AAC Asn | CCT Pro 175 | TTG Leu | | 528 |
| GGA Gly | CGC Arg | ACC Thr | GTG Val 180 | ATG Met | TTA Leu | ACG Thr | GTT Val | CAG Gln 185 | TTC Phe | ACT Thr | CTC Leu | GGC Gly | TGG Trp 190 | CCG Pro | TTG Leu | • | 576 |
| TAC Tyr | TTA Leu | GCC Ala 195 | TTC Phe | AAC Asn | GTC Val | TCG Ser | GGA Gly 200 | AGA Arg | CCT Pro | TAC Tyr | GAC Asp | GGC Gly 205 | GGC Gly | TTC Phe | CGT Arg | ٠. | 624 |
| TGC Cys | CAT His 210 | TTC Phe | CAC His | CCC Pro | AAC Asn | GCT Ala 215 | CCC | ATC Ile | TAC Tyr | AAC Asn | GAC Asp 220 | CGC Arg | GAG Glu | CGT Arg | CTC Leu | | 672 |
| CAG Gln 225 | ATA Ile | TAC Tyr | ATC Ile | TCC Ser | GAC Asp 230 | GCT Ala | GGC Gly | ATC Ile | CTC Leu | GCC Ala 235 | GTC Val | TGC Cys | TAC Tyr | GGT Gly | CTC Leu 240 | | 720 |
| TTC Phe | CGT Arg | TAC Tyr | GCC Ala | GCC Ala 245 | GGC Gly | CAG Gln | GGA Gly | GTG Val | GCC Ala 250 | TCG Ser | ATG Met | GTC Val | TGC Cys | TTC Phe 255 | TAC Tyr | | 768 |
| GGA Gly | GTC Val | CCG Pro | CTT Leu 260 | CTĠ Leu | ATT | GTC Val | AAT Asn | GGT Gly 265 | TTC Phe | CTC Leu | GTG Val | TTG Leu | ATC Ile 270 | ACT Thr | TAC | | 816 |
| TTG Leu | CAG Gln | CAC His 275 | ACG Thr | CAT His | CCT Pro | TCC | CTG Leu 280 | Pro | CAC | TAC Tyr | GAT Asp | TCG Ser 285 | Ser | GAG Glu | TGG Trp | | 864 |
| GAT Asp | TGG Trp 290 | TTC Phe | AGG Arg | GGA Gly | GCT Ala | TTG Leu 295 | Ala | ACC Thr | GTT Val | GAC Asp | AGA Arg 300 | Asp | TAC Tyr | GGA Gly | ATC Ile | | 912 |
| TTG Leu 305 | AAC Asn | AAG Lys | GTC Val | TTC Phe | CAC His 310 | Asn | ATT Ile | ACC Thr | GAC Asp | ACG Thr | His | GTG Val | GCC Ala | CAT His | CAT His 320 | | 960 |
| CCG Pro | TTC Phe | TCC Ser | ACG Thr | ATG Met 325 | Pro | CAT His | TAT Tyr | CAC His | GCG Ala 330 | Met | GAA Glu | GCT Ala | ACC Thr | AAC Lys | GCG Ala | | 1008 |
| ATA Ile | AAG Lys | CCG Pro | ATA Ile 340 | Leu | GGA Gly | GAG Glu | TAT | TAT | Gln | TTC Phe | GAT Asp | GGC Gly | ACG Thr 350 | Pro | G GTG Val | | 1056 |
| GTT Val | AAG Lys | GCG Ala 355 | Met | TGG Trp | AGG Arg | GAG Glu | GCG Ala 360 | Lys | GAG Glu | TGI Cys | ATC | TATE TYPE | r Val | GAA L Glu | A CCG | | 1104 |
| | | | | | | | | | | | | | | | | | |

GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
370 375 380

GA

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 15

Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 55 60

Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 140.

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175

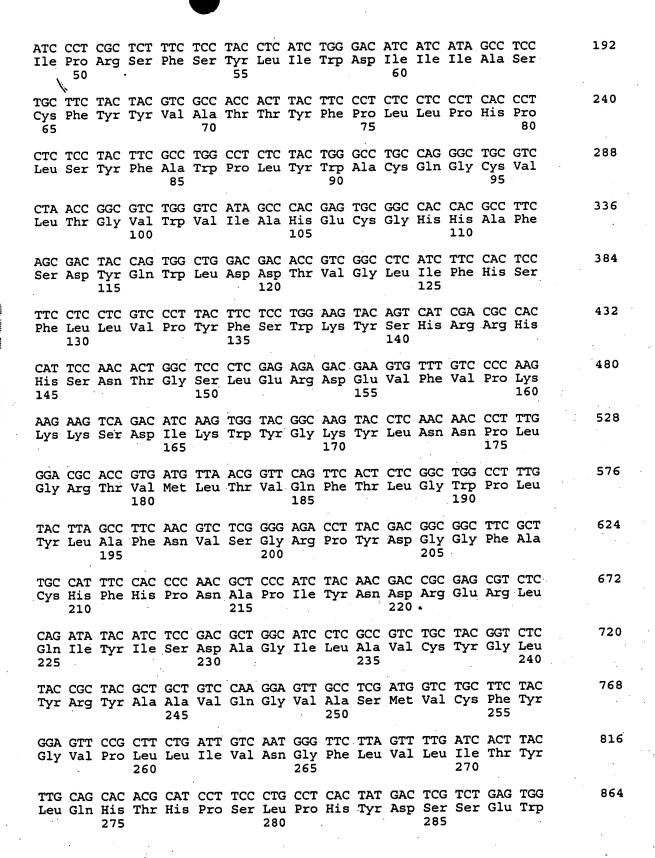
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg 195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240

| Phe | Arg | Tyr | Ala | Ala 245 | Gly | Gln | Gly | Val | Ala 250 | Ser | Met | Val | Cys | Phe 255 | Tyr | | • • • |
|------------------|------------|-----------------|--------------------------------------|--------------------------------------|-------------------------------------|---------------------------------------------------------|-----------------------------------|----------------------|------------------|------------|--------------|------------|----------------|----------------------|------------|-----|-------|
| Gly [\] | Val | Pro | Leu 260 | Leu | Ile | Val | Asn | Gly 265 | Phe | Leu | Val | Leu | Ile 270. | Thr | Tyr | ٠ | |
| Leu | Gln | His 275 | Thr | His | Pro | Ser | Leu 280 | Pro | His | Tyr | Asp | Ser 285 | Ser | Glu | Trp | | |
| | Trp 290 | Phe | Arg | Gly | Ala | Leu 295 | Ala | Thr | Val | Asp | Arg 300 | Asp | Tyr | Gly | Ile | | |
| Leu 305 | Asn | Lys | Val | Phe | His 310 | Asn | Ile | Thr | Asp | Thr 315 | His | Val | Ala | His | His 320 | | |
| Pro | Phe | Ser | Thr | Met 325 | Pro | His | Tyr | His | Ala 330 | Met | Glu | Ala | Thr | Lys 335 | Ala | | |
| Ile | Lys | Pro | Ile 340 | Leu | Gly | Glu | Tyr | Tyr 345 | Glń | Phe | Asp | Gly | Thr 350 | Pro | Val | • | * |
| Val | Lys | Ala 355 | Met | Trp | Arg | Glu | Ala 360 | Lys | Glu | Cys | Ile | Tyr 365 | Val | Glu | Pro | | 0 |
| Asp | Arg 370 | Gln | Gly | Glu | Lys | Lys 375 | Gly | Val | Phe | Trp | Tyr 380 | Asn | Asn | Lys | Leu | • | · |
| | (i; |) SE (. (| QUEN A) L B) T C) S D) T | CE C ENGT YPE: TRAN OPOL | HARA H: 1 nuc DEDN OGY: | ON FO CTER 155 leic leic ESS: lin DNA | ISTI base aci sin ear | CS: pai d | | - | | | | | | | |
| | | | | ETIC | | | | • | | | | | | | | | |
| • | (iv |) AN | TI-S | ENSE | : NO |): | | | | | | | | | | | |
| | (vi | | | AL S | | E: Bra | ssic | a na | pus | | • | • | | | | | |
| | (ix |) FE (| ATUR D) O | E: THER | INF | ORMA | TION | J: Wi | ld t | ype | Fad2 | 2 •, | | | | : % | |
| | (xi |) SE | QUEN | ICE I | ESCR | IPTI | ON: | SEQ | ID N | 10 : 5 : | | | | | | | |
| ATG Met | Gly | GCA Ala | GGT | GGA Gly | AGA Arg | ATG Met | G CA | A GTO | TCT Ser 10 | Pro | CCC Pro | TC0 Sei | C AAA | A AAC 5 Lys 19 | TCT Ser | ÷ | 48 |
| GAA Glu | ACC | GAC Asp | AAC Asr | ı Ile | AAC Lys | G CGC | GT/ Va | A CCC l Pro 25 | Cys | C GAG | ACI 1 Th: | A CCC | G CCC D Pro | o Phe | ACT Thr | ٠ | 96 |
| GTC Val | | CNZ | COC | י אאר | | | 1 1 m | | | | | T (T) | מא יי | | - maa | | 144 |



| GAT Asp | TGG Trp 290 | TTG Leu | AGG Arg | GGA Gly | GCT Ala | TTG Leu 295 | GCC Ala | ACC Thr | GTT Val | GAC Asp | AGA Arg 300 | GAC Asp | TAC Tyr | GGA Gly | ATC Ile | | 912 |
|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|---|------|
| TTG Leu 305 | AAC Asn | AAG Lys | GTC Val | TTC Phe | CAC His 310 | AAT Asn | ATC Ile | ACG Thr | GAC Asp | ACG Thr 315 | CAC His | GTG Val | GCG Ala | CAT His | CAC His 320 | | 960 |
| | | | | | | | | | | | GAA Glu | | | | Ala | | 1008 |
| ATA Ile | AAG Lys | CCG Pro | ATA Ile 340 | CTG Leu | GGA Gly | GAG Glu | TAT Tyr | TAT Tyr 345 | CAG Gln | TTG Leu | CAT His | GGG Gly | ACG Thr 350 | CCG Pro | GTG Val | | 1056 |
| GTT Val | AAG Lys | GCG Ala 355 | ATG Met | TGG Trp | AGG Arg | GAG Glu | GCG Ala 360 | AAG Lys | GAG Glu | TGT | ATC Ile | TAT Tyr 365 | GTG Val | GAA Glu | CCG Pro | | 1104 |
| GAC Asp | AGG Arg 370 | CAA Gln | GGT Gly | GAG Glu | AAG Lys | AAA Lys 375 | GGT Gly | GTG Val | TTC Phe | TGG Trp | TAC Tyr 380 | AAC Asn | AAT Asn | AAG Lys | TTA Leu | T | 1153 |
| GA | | | | | | | | | | | | | | | | | 1155 |

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240

Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 255

Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
275 280 285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 305 310 315

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile.Tyr Val Glu Pro 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 370 375 380

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

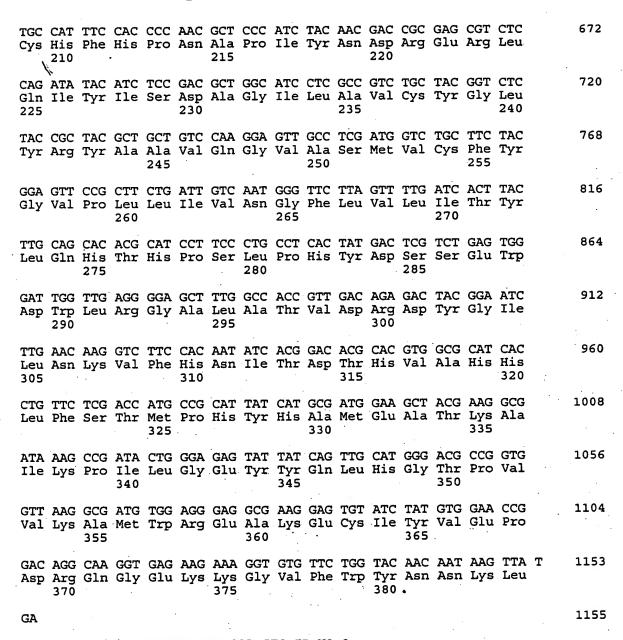
(vi) ORIGINAL SOURCE: (A) ORGANISM: Brassica napus

(ix) FEATURE:

(D) OTHER INFORMATION: T to A transversion mutation at nucleotide 515.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | (71) | 200 | SOPIAC | | | | | v | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|-----|--|
| ATG Met 1 | GGT Gly | GCA Ala | GGT Gly | GGA Gly 5 | AGA Arg | ATG Met | CAA Gln | GTG Val | TCT Ser 10 | CCT Pro | CCC Pro | TCC Ser | AAA Lys | AAG Lys 15 | TCT Ser | | 48 | |
| GAA Glu | ACC Thr | GAC Asp | AAC Asn 20 | ATC Ile | AAG Lys | CGC Arg | GTA Val | CCC Pro 25 | TGC Cys | GAG Glu | ACA Thr | CCG Pro | CCC Pro 30 | TTC Phe | ACT Thr | • | 96 | |
| GTC Val | GGA Gly | GAA Glu 35 | CTC Leu | AAG Lys | AAA Lys | GCA Ala | ATC Ile 40 | Pro | CCG Pro | CAC His | TGT Cys | TTC Phe 45 | AAA Lys | CGC Arg | TCG Ser | | 144 | |
| ATC Ile | CCT Pro 50 | CGC Arg | TCT Ser | TTC Phe | TCC Ser | TAC Tyr 55 | CTC Leu | ATC Ile | TGG Trp | GAC Asp | ATC Ile 60 | ATC Ile | ATA Ile | GCC Ala | TCC Ser | • | 192 | |
| TGC Cys 65 | TTC Phe | TAC Tyr | TAC Tyr | GTC Val | GCC Ala 70 | ACC Thr | ACT Thr | TAC Tyr | TTC Phe | CCT Pro 75 | CTC Leu | CTC Leu | CCT Pro | CAC | CCT Pro 80 | X . | 240 | |
| CTC Leu | TCC Ser | TAC Tyr | TTC Phe | GCC Ala 85 | TGG Trp | CCT Pro | CTC Leu | TAC Tyr | TGG Trp 90 | GCC Ala | TGC Cys | CAG Gln | GGC | TGC Cys 95 | GTC Val | | 288 | |
| CTA Leu | ACC Thr | GGC Gly | GTC Val 100 | TGG Trp | GTC Val | ATA Ile | GCC Ala | CAC His 105 | GAG Glu | TGC Cys | GGC Gly | CAC His | CAC His 110 | Ala | TTC Phe | | 336 | |
| AGC Ser | GAC Asp | TAC Tyr 115 | Gln | TGG Trp | CTG Leu | GAC Asp | GAC Asp 120 | ACC Thr | GTC Val | GGC Gly | CTC Leu | ATC Ile 125 | Phe | CAC | TCC Ser | | 384 | |
| TTC Phe | CTC Leu 130 | Leu | GTC Val | CCT Pro | TAC Tyr | TTC Phe 135 | TCC | TGG Trp | AAG Lys | TAC Tyr | AGT Ser 140 | His | CGA Arg | CGC Arg | CAC His | | 432 | |
| CAT His 145 | TCC Ser | AAC Asn | ACT Thr | GGC Gly | TCC Ser 150 | Leu | GAG Glu | AGA Arg | GAC Asp | GAA Glu 155 | Val | TTT Phe | GTC Val | CCC | AAG Lys 160 | | 480 | |
| AAG Lys | AAG Lys | TCA Ser | GAC Asp | ATC Ile 165 | Lys | TGG Trp | TAC | GGC | AAG Lys 170 | Tyr | CAC | AAC Asn | AAC Asn | CCT Pro 175 | TTG | | 528 | |
| GGA Gly | CGC Arg | ACC Thr | GTG Val 180 | Met | TTA Leu | ACG Thr | GTI Val | CAG Gln 185 | Phe | ACT Thr | CTC Lev | GGC Gly | TGG Trp | Pro | TTG Leu | | 576 | |
| TAC | TTA Leu | GCC Ala 195 | Phe | AAC Asn | GTC Val | TCG Ser | GGG Gly 200 | Arg | CCT Pro | TAC Tyr | GAC Asp | GGG Gly 205 | GTA | TTC Phe | GCT Ala | | 624 | |
| | | | | | | | | | | | | | | | | | | |



(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 30

- Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 80 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 Typ Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Rep Leu Leu Val Pro Tyr Phe Ser Typ Lys Tyr Ser His Arg Arg His
- Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 130 135 140
- His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160
- Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu 165 170 175
- Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190
- Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 195 200 205
- Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220
- Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240
- Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 255
- Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 270
- Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 275 280 285
- Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300
- Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 305 310 315 320
- Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335
- Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val 340 345 350
- Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 375 380 370

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...1152

 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | GGA Gly 5 | | | | | | | | 4 | 8 |
|--|------|------------------|------|------|------|---|--|-----|-------------------|----|----|
| | | ATC Ile | | | | | | | | 9 | 96 |
| | | AAG Lys | | | | | | | | 14 | 14 |
| | | TTC Phe | | | | | | | | 19 | 92 |
| | | GTC Val | | | | - | | | | 24 | 10 |
| | | GCC Ala 85 | | | | | | | | 28 | 88 |
| | | TGG Trp | | | | | | | | 3: | 36 |
| | | TGG Trp | | | | | | | TCC Ser | 31 | 84 |
| | | CCT Pro | | | | | | | | 4: | 32 |
| | | GGC Gly | | | | | | Pro | AAG Lys 160 | 4 | 80 |
| | | | | | | | | | | | |





| | AAG Lys | | | | | | | | | | | | | | | | 528 |
|------------|-------------------|------------|-------------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|-------------------|------------|------------|-----|------|
| | CGC Arg | | | | | | | | | | | | | | | | -576 |
| | TTA Leu | | | | | | | | | | | | | | | | 624 |
| | CAT His 210 | | | | | | | | | | | | | | | | 672 |
| | ATA Ile | | | | | Ala | | | | | | | | | | | 720 |
| | CGC Arg | | | | | | | | | | | | | | | | 768 |
| | GTT Val | | | | | | | | | | | | | | | : | 816 |
| | CAG Gln | | | | | | | | | | | | | | | • | 864 |
| | TGG Trp 290 | | | | | | | | | | | | | | | . * | 912 |
| | AAC Asn | | | | | | | | | | | | | | | | 960 |
| | TTC Phe | | | | | | | | | | | | | | | | 1008 |
| ATA Ile | AAG Lys | CCG Pro | ATA Ile 340 | CTG Leu | GGA Gly | GAG Glu | TAT Tyr | TAT Tyr 345 | CAG Gln | TTC Phe | GAT Asp | GGG Gly | ACG Thr 350 | CCG Pro | GTG Val | | 1056 |
| | AAG Lys | | | | | | | | | | | | | | | | 1104 |
| | AGG Arg 370 | | | | | | | | | | | | | | | T | 1153 |
| GA | | | | | | | | | | | | | | | | | 1155 |



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

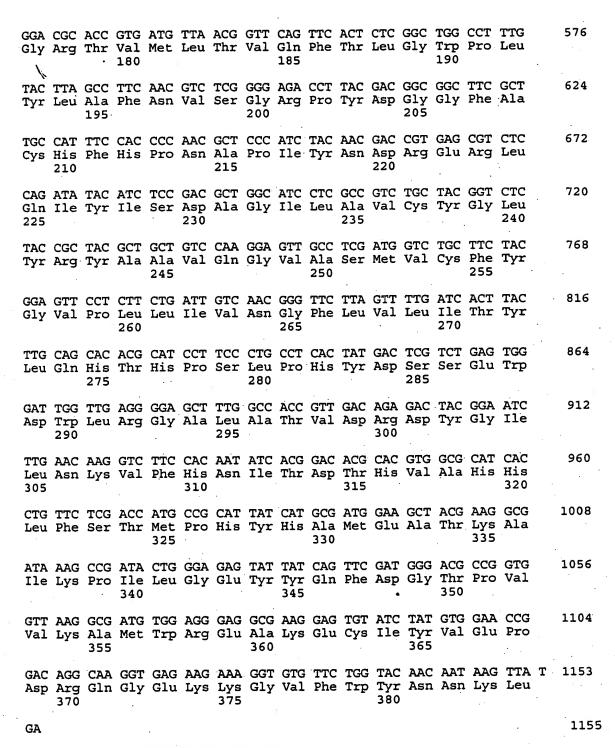
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 105 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 115 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 140 135 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 155 150 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 200 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 215 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 235 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 250 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 265 260 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 295 300 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 310 315 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 345 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 360 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 380

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| ATG Met 1 | GGT Gly | GCA Ala | GGT Gly | GGA Gly 5 | AGA Arg | ATG Met | CAA Gln | GTG Val | TCT Ser 10 | CCT Pro | CCC Pro | TCC Ser | AAA Lys | AAG Lys 15 | TCT Ser | | 48 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------------|-----|
| GAA Glu | ACC Thr | GAC Asp | AAC Asn 20 | ATC Ile | AAG Lys | CGC Arg | GTA Val | CCC Pro 25 | TGC Cys | GAG Glu | ACA Thr | CCG Pro | CCC Pro 30 | TTC Phe | ACT Thr | | ,96 |
| GTC Val | GGA Gly | GAA Glu 35 | CTC Leu | AAG Lys | AAA Lys | GCA Ala | ATC Ile 40 | CCA Pro | CCG Pro | CAC His | TGT Cys | TTC Phe 45 | AAA Lys | CGC Arg | TCG Ser | ; ; ; ; ; ; | 144 |
| ATC Ile | CCT Pro 50 | CGC Arg | TCT. Ser. | TTC Phe | TCC Ser | TAC Tyr 55 | CTC Leu | ATC Ile | TGG Trp | GAC Asp | ATC Ile 60 | ATC Ile | ATA Ile | GCC Ala | TCC Ser | | 192 |
| TGC Cys 65 | TTC Phe | TAC Tyr | TAC Tyr | GTC Val | GCC Ala 70 | ACC Thr | ACT Thr | TAC Tyr | TTC Phe | CCT Pro 75 | CTC Leu | CTC Leu | CCT Pro | CAC His | CCT Pro 80 | | 240 |
| CTC Leu | TCC Ser | TAC Tyr | TTC Phe | GCC Ala 85 | TGG Trp | CCT Pro | CTC Leu | TAC Tyr | TGG Trp 90 | GCC Ala | TGC Cys | CAG Gln | GGC Gly | TGC Cys 95 | GTC Val | ٠. | 288 |
| CTA Leu | ACC Thr | GGC Gly | GTC Val 100 | TGG Trp | GTC Val | ATA Ile | GCC Ala | CAC His 105 | AAG Lys | TGC Cys | GGG Gly | CAC His | CAC His 110 | Ala | TTC Phe | | 336 |
| AGC Ser | GAC Asp | TAC Tyr 115 | CAG Gln | TGG Trp | CTG Leu | GAC Asp | GAC Asp 120 | ACC Thr | GTC Val | GGC Gly | CTC Leu | ATC Ile 125 | TTC Phe | CAC His | TCC. Ser | | 384 |
| TTC Phe | CTC Leu 130 | Leu | GTC Val | CCT Pro | TAC Tyr | TTC Phe 135 | TCC Ser | TGG Trp | AAG Lys | TAC | AGT Ser 140 | His | CGA Arg | CGC | CAC His | | 432 |
| CAT His 145 | Ser | AAC Asn | ACT Thr | GGC Gly | TCC Ser 150 | Leu | GAG Glu | AGA Arg | GAC Asp | GAA Glu 155 | Val | TTT Phe | GTC Val | CCC Pro | AAG Lys 160 | | 480 |
| AAG Lys | AAG Lys | TCA Ser | GAC Asp | ATC Ile 165 | Lys | TGG | TAC | GGC | AAG Lys 170 | Tyr | CTC Leu | AAC Asn | AAC Asn | CCT Pro 175 | TTG Leu | | 528 |
| | | | | | | | | | | | | | | | | | |



(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

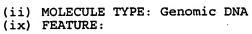
(ii) MOLECULE TYPE: protein (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
                        55
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
                                    90
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
                                105
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
                            120
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
                                            140
                        135
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                                       155
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                                    170
                165
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
                                                     190
            180
                                185
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
                            200
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                                             220
                        215
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
                                        235
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
                                    250
                245
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
                                265
            260
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
                            280
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
                                             300
                        295
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
                                        315
                    310
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
                                                         335
                                    330
                325
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
                                                     350
                                 345
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
                                                 365
                            360
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
                                             380
```

(2) INFORMATION FOR SEQ ID NO:13:

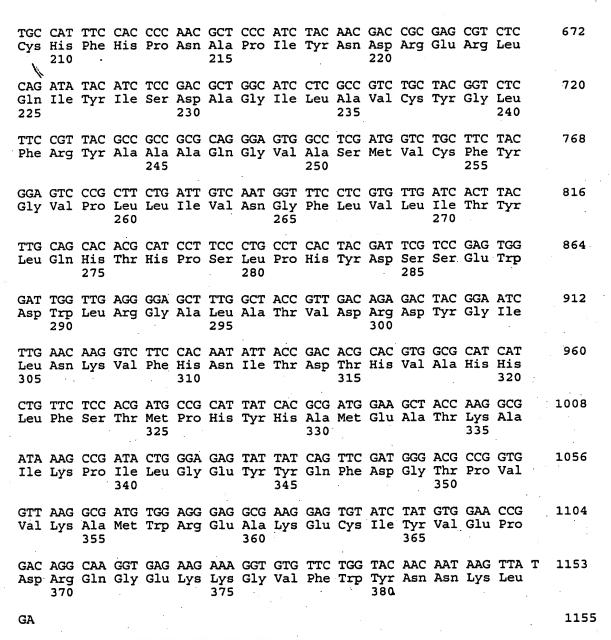
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



(A) NAME/KEY: Coding Sequence (B) LOCATION: 1...1152 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

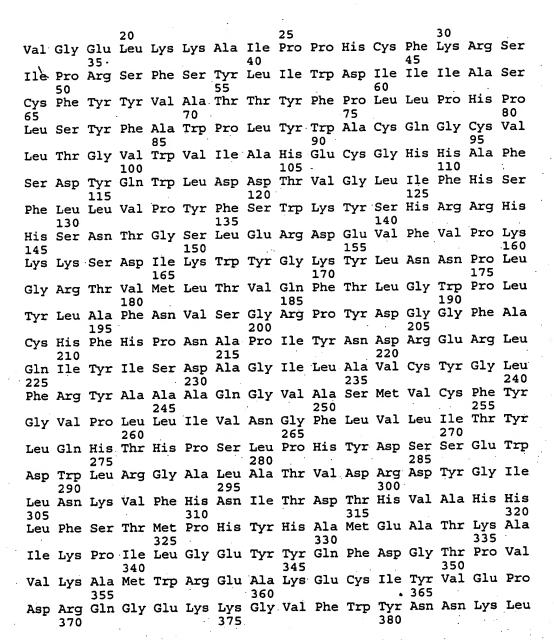
| | G GGT | | | | | | | | | | | | | | | | 48 |
|----------|-----------------------|-------------------|-------------------|------------|------------|------------|-------------------|-------------------|------------|------------|------------|-------------------|-------------------|------------|------------|----|-----|
| GA G1 | A ACC | GAC Asp | ACC Thr 20 | ATC Ile | AAG Lys | CGC Arg | GTA Val | CCC Pro 25 | TGC Cys | GAG Glu | ACA Thr | CCG Pro | CCC Pro 30 | TTC Phe | ACT Thr | | 96 |
| | C GGA l Gly | | | | | | | | | | | | | | | | 144 |
| | C CCT Pro 50 | | | | | | | | | | | | | | | | 192 |
| | C TTC s Phe | | | | | | | | | | | | | | | : | 240 |
| | C TCC u Ser | | | | | | | | | | | | Gly | | | | 288 |
| | A ACC u Thr | | | | | | | | | | | | | | | | 336 |
| AG Se | C GAC r Asp | TAC Tyr 115 | CAG Gln | TGG Trp | CTT Leu | GAC Asp | GAC Asp 120 | ACC Thr | GTC Val | GGT Gly | CTC Leu | ATC Ile 125 | TTC Phe | CAC His | TCC Ser | | 384 |
| | C CTC e Leu 130 | | | | | | | | | Tyr | | | | | | | 432 |
| | T TCC s Ser 5 | | | | | Leu | | | | | | | | | | • | 480 |
| | G AAG s Lys | | | | | | | | | | | | | | | x. | 528 |
| GG G1 | A CGC y Arg | ACC | GTG Val 180 | ATG Met | TTA Leu | ACG Thr | GTT Val | CAG Gln 185 | TTC Phe | ACT Thr | CTC Leu | GGC Gly | TGG Trp 190 | CCG Pro | TTG Leu | | 576 |
| | C TTA r Leu | | Phe | | | | | Arg | | | | | Gly | | | | 624 |



(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr



(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152
 - (D) OTHER INFORMATION:





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | AGA Arg | | | | | | | | | | | | 48 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----|-----|
| | | | | | AAG Lys | | | | | | | | | | | | 96 |
| | | | | | AAA Lys | | | | | | | | | | | | 144 |
| | | | | | TCC Ser | | | | | | | | | | | | 192 |
| | | | | | GCC Ala 70 | | | | | | | | | | | | 240 |
| | | | | | TGG Trp | | | | | | | | | | | | 288 |
| | | | | | GTC Val | | | | | | | | | | | ** | 336 |
| AGC Ser | GAC Asp | TAC Tyr 115 | CAG Gln | TGG Trp | CTT | GAC Asp | GAC Asp 120 | ACC Thr | GTC Val | GGT | CTC Leu | ATC Ile 125 | TTC Phe | CAC His | TCC | | 384 |
| TTC Phe | CTC Leu 130 | CTC Leu | GTC Val | CCT Pro | TAC Tyr | TTC Phe 135 | TCC Ser | TGG Trp | AAG Lys | TAC | AGT Ser 140 | CAT His | CGA Arg | CGC Arg | CAC His | | 432 |
| | | | | | TCC Ser 150 | | | | | | | | | | | | 480 |
| AAG Lys | AAG Lys | TCA Ser | GAC Asp | ATC Ile 165 | AAG Lys | TGG Trp | TAC Tyr | GGC Gly | AAG Lys 170 | TAC | CAG His | AAC Asn | AAC Asn | CCT Pro 175 | TTG Leu | | 528 |
| GGA Gly | CGC | ACC Thr | GTG Val 180 | ATG Met | TTA Leu | ACG Thr | GTT Val | CAG Gln 185 | TTC Phe | ACT Thr | CTC Leu | GGC Gly | TGG Trp 190 | Pro | TTG Leu | | 576 |
| | | | Phe | | | | | | | | | | Gly | | GCT Ala | | 624 |
| | | | | | | | | | | | | | | | CTC Leu | | 672 |
| CAG Gln 225 | Ile | TAC Tyr | ATC Ile | TCC Ser | GAC Asp 230 | Ala | GGC Gly | ATC Ile | CTC Leu | GCC Ala 235 | Val | TGC Cys | TAC | GGT | CTC Leu 240 | | 720 |





| TTC Phe | CGT Arg | TAC Tyr | GCC Ala | GCC Ala 245 | Ala | CAG Gln | GGA Gly | GTG Val | GCC Ala 250 | TCG Ser | ATG Met | GTC Val | TGC Cys | TTC Phe 255 | TAC Tyr | | 768 |
|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|---|------|
| GGA Gly | GTC Val | Pro | CTT Leu 260 | CTG Leu | ATT Ile | GTC Val | AAT Asn | GGT Gly 265 | TTC Phe | CTC Leu | GTG Val | TTG Leu | ATC Ile 270 | ACT Thr | TAC Tyr | | 816 |
| | | | | CAT His | | | | | | | | | | | TGG Trp | | 864 |
| | | | | GGA Gly | | | | | | | | | | | | | 912 |
| | | | | TTC Phe | | | | | | | | | | | | | 960 |
| | | | | ATG Met 325 | | | | | | | | | | | | | 1008 |
| | | | | CTG Leu | | | | | | | | | | | GTG Val | | 1056 |
| GTT Val | AAG Lys | GCG Ala 355 | ATG Met | TGG Trp | AGG Arg | GAG Glu | GCG Ala 360 | AAG Lys | GAG Glu | TGT Cys | ATC Ile | TAT Tyr 365 | GTG Val | GAA Glu | CCG Pro | | 1104 |
| GAC Asp | AGG Arg 370 | CAA Gln | GGT Gly | GAG Glu | AAG Lys | AAA Lys 375 | GGT Gly | GTG Val | TTC Phe | TGG | TAC Tyr 380 | Asn | AAT Asn | AAG Lys | TTA Leu | Ť | 1153 |
| GA | | | | | | | | • | | | | | • | | | | 1155 |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

 Met
 Gly
 Ala
 Gly
 Gly
 Arg
 Met
 Gln
 Val
 Ser
 Pro
 Pro
 Ser
 Lys
 Lys
 Ser

 Glu
 Thr
 Asp
 Thr
 Ile
 Lys
 Arg
 Val
 Pro
 Cys
 Glu
 Thr
 Pro
 Pro





Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 105 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 140 135 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 150 155 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu 170 165 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 195 200 205 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230. 235 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 265 260 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 315 310 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 340 345 350 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 360 365 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 375 370 . 380

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

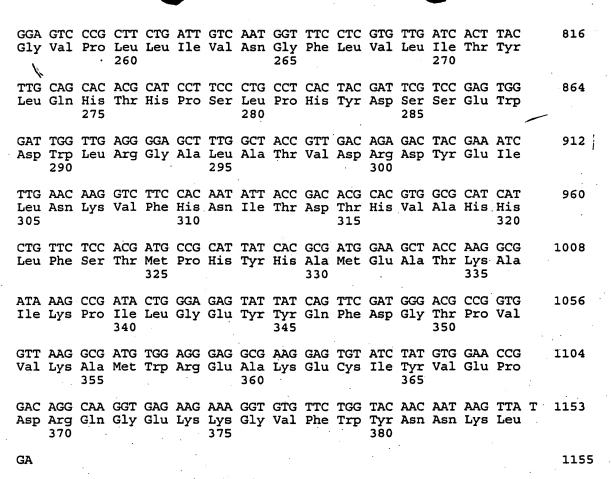
ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15

48





| | | | | | | | | | | | ACA Thr | | | | | | 96 |
|------------|-------------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|---|-----|
| | | | | | | | | | | | TGT Cys | | | | TCG Ser | | 144 |
| | | | | | | | | | | | ATC Ile 60 | | | | | | 192 |
| | | | | | | | | | | | CTC Leu | | | | | | 240 |
| | | | | | | | | | | | TGC Cys | | | | | | 288 |
| | | | | | | | | | | | GGC | | | | | | 336 |
| | | | | | | | | | | | CTC | | | | TCC Ser | | 384 |
| TTC Phe | CTC Leu 130 | CTC Leu | GTC Val | CCT Pro | TAC Tyr | TTC Phe 135 | TCC Ser | TGG Trp | AAG Lys | TAC Tyr | AGT Ser 140 | CAT His | CGA Arg | CGC Arg | CAC His | | 432 |
| | | | | | | | | | | | GTG Val | | | | | | 480 |
| | | | | | Lys | | | | | | CTC Leu | | | | Leu | | 528 |
| | | | | | | | | | | | CTC Leu | | | | TTG Leu | | 576 |
| | | | | | | | | | | | GAC Asp | | | | | - | 624 |
| | | | | | | | | | | | GAC Asp 220 | | | | | • | 672 |
| | | | | | | | | | | | GTC Val | | | | | | 720 |
| | | | | | | | | Val | | | ATG Met | | | | | • | 768 |



(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

 Met
 Gly
 Ala
 Gly
 Arg
 Met
 Gln
 Val
 Ser
 Pro
 Pro
 Ser
 Lys
 Lys
 Ser

 Glu
 Thr
 Asp
 Thr
 Ile
 Lys
 Arg
 Val
 Pro
 Cys
 Glu
 Thr
 Pro
 Pro





Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 135 140 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 150 155 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 190 185 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 200 205 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 215 220 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 235 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Glu Ile 295 300 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 315 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 345 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 360 365 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 375 380

- (2) INFORMATION FOR SEQ ID NO:19:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other Nucleic Acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATATGATG ATGGTGAAAG A

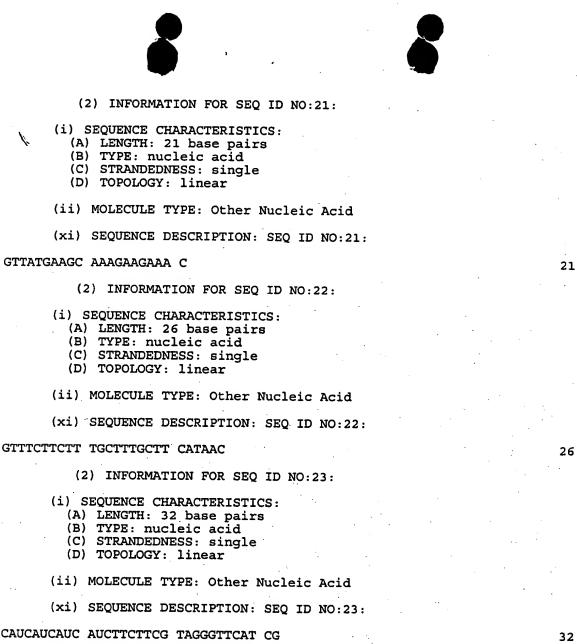
(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other Nucleic Acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCTTTCACCA TCATCATATC C

21

21



- (ii) MOLECULE TYPE: Other Nucleic Acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

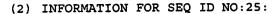
CAUCAUCAUC AUCTTCTTCG TAGGGTTCAT CG

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other Nucleic Acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CUACUACUAC UATCATAGAA GAGAAAGGTT CAG





- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAUCAUCAUC AUCATGGGTG CACGTGGAAG AA

- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CUACUACUAC UATCTTTCAC CATCATCATA TCC

33

32